

AMENDMENTS TO THE SPECIFICATION

Please replace the first full paragraph on page 14 of the specification, beginning at line 7, with the following amended paragraph:

Another method for modifying plant growth characteristics resides in the use of allelic variants of a gene essentially similar to SEQ ID NO 1. Allelic variants exist in nature and encompassed within the methods of the present invention is the use of these natural alleles. "Allelic variants" are defined herein comprise single nucleotide polymorphisms (SNPs) as well as small insertion/deletion polymorphisms (INDELs ; the size of INDELs is usually less than 100 bp). SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms. Differences between alleles are naturally occurring differences between the genes of different plants of the same species. These differences may be substitution and/or addition and/or deletion of for example 1, 2, 3 or more base pairs. The allelic variant preferably encodes a protein comprising the motif according to SEQ ID NO: 32: FFXXLLPPII FFXXLLPPII, where X can be any amino acid and/or Na⁺/H⁺ activity.

Please replace the paragraph which bridges pages 25 and 26 of the specification with the following amended paragraph:

~~FIG. 3 is an alignment from Yokoi et al., 2002 showing six Arabidopsis thaliana isogenes~~ (AtNHX) encoding proteins that have domains with sequence similarity to metazoan NHE Na⁺/H⁺ exchangers. The predicted peptides from AtNHX1 (AF106324), AtNHX2 (AC009465), AtNHX3 (AC0011623), AtNHX4 (AB015479), AtNHX5 (AC005287) and AtNHX6 (AC010793) are aligned based on analysis using the CLUSTAL V method (Higgins and Sharp, 1989). As set forth in the Yokoi et al., 2002 publication, residues ~~Residues~~ that are identical in all AtNHX family members are highlighted in black, those identical in subgroup 1 family members (AtNHX1.-4) are shaded in dark grey, and those residues speci/Ec to the subgroup 2 family members (AtNHX5 and 6) are highlighted in light grey. Putative transmembrane domains are indicated by Roman numerals. The consensus amiloride binding motif is indicated in transmembrane domain III.

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Please amend the first full paragraph on page 26 of the specification by substituting the following amended paragraph:

Fig. 3 ~~Fig.~~4 lists examples of sequences useful in the methods of the invention.